

NEB 1233
 -1391 -1381 -1371 -1361 -1351 -1341 -1331 -1321 *
 * * * * * * * *
AGGGGATAAC AATTTCACAC AGGAAACAGC TATGGAOCAT ATTAGCCAA GCTTGGTACG GAGCTCGATG CCACTAGTAA
pCR2.1 _____> BamHI _____>
Lac promoter _____>
 -1311 -1301 -1291 -1281 -1271 -1261 -1251 -1241 *
 * * | * * * * * *
GGGCCCGAC TGTGCTGAA TTGGCTTAC TATAGCCAC CGGTGGTGA CGCCCGGGC TGTTAACCTT AAGAGAAATT
pCR2.1 _____> SmaI _____>
GenomeWalker Adaptor _____> craCO1 _____>
 -1231 -1221 -1211 -1201 -1191 -1181 -1171 -1161 *
 * * * * * * * *
GGTAAAATTC CTAGAGGAA TTGTAATIAA TATGGAGAA TGATTTAT TCTAAITGTT TATCCATTIT CGRTAAAGIT
craCO1 Genomic DNA _____>
 -1151 -1141 -1131 -1121 -1111 -1101 -1091 -1081 *
 * * * * * * * *
AAATAAAGTG TGTTAGACGA CCATCATCT TAATCCATT GTACTTTCAT AAATTGTTAC TGAGATTTAA GTICAATTC
craCO1 Genomic DNA _____>
 -1071 -1061 -1051 -1041 -1031 -1021 -1011 -1001 *
 * * * * * * * *
ACACTAAAC AATGAAAAG TATGGACAA TCACAAATGGA AAATACGTTA GATGTTACCC ATCACCTTC AAGTCTAAC
craCO1 Genomic DNA _____>
 -991 -981 -971 -961 -951 -941 -931 -921 *
 * * * * * * * *
CTAGGATAT TTTGGATAA TTGAGMTTT ATTAAATAT TCITITATOC GTTGACAGTT TAITTTTGT TAAAGGAGT
craCO1 Genomic DNA _____>
 -911 -901 -891 -881 -871 -861 -851 -841 *
 * * * * * * * *
ATGTAAGAA CGACGAAATA TGTTAAATAA CCAAGATGC ATACAATAA GAGCTAGTTC CTAAAGATAT ATAAAAGTAT
craCO1 Genomic DNA _____>
 -831 -821 -811 -801 -791 -781 -771 -761 *
 * * * * * * * *
GTCACACAC GTACAAAAACG TTTCCTTTCG ATGATAATAA TCTTAAAGAC TTCAAGGTTA ATTAGATCT CTTAATTAAA
craCO1 Genomic DNA _____>
 -751 -741 -731 -721 -711 -701 -691 -681 *
 * * * * * * * *
AAATTCTATA GATAATGCAAT CGGTGACAA GAAAAACAT AAAGACCCA TGGTGTGCTT ATTITTTGTA GTAATTAAGC
craCO1 Genomic DNA _____>
 -661 -651 -641 -631 -621 -611 -601 -591 *
 * * * * * * * *
GDAGTCAAG ACACAAAGTAA GAATGAGCTT ACCACATGTT ATATGAGTT CCAAAGTCT AGCTTGTGAG CACGTTACCA
craCO1 Genomic DNA _____>

Fig. 1A

G
G
G
G
G
G
G
G
G

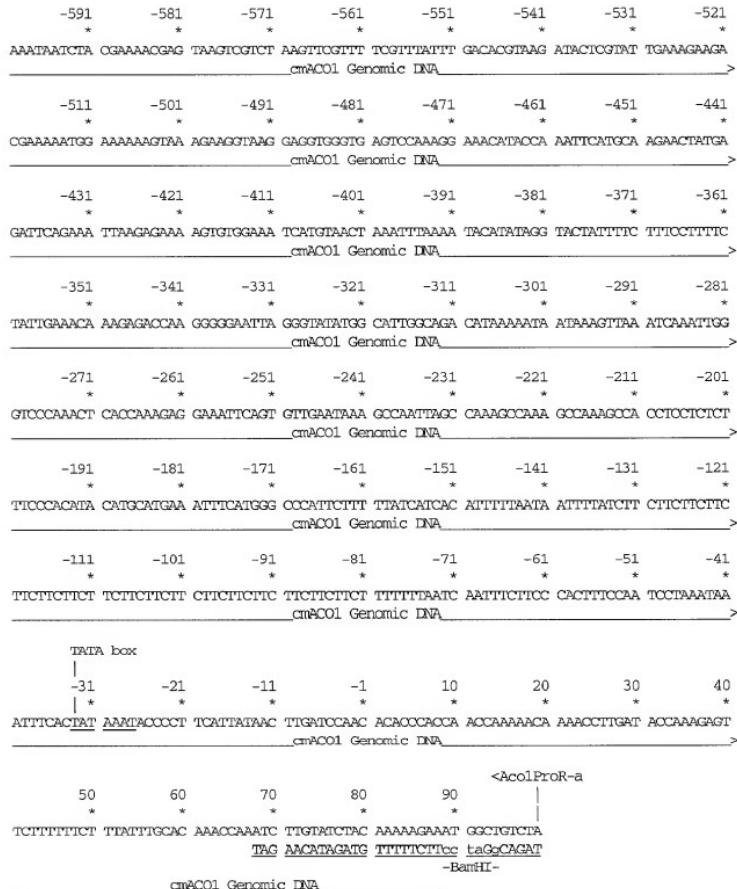


Fig. 1B

-1289 -1279 -1269 -1259 -1249 -1239 -1229 -1219
 * * * * * * * *
 AGGAACAGC TATGACCATG ATTACCCCAA GCCTTAAGAGA AATTTGGTAA ATTCTCTAGAG AGAATTGTAA TTAATATAGG
 HindIII
 pUC19 _____ cmrCO1 Genomic DNA >
 -1209 -1199 -1189 -1179 -1169 -1159 -1149 -1139
 * * * * * * * *
 AGAAATGATT TAATTCCTAA GTTGTATCCA TTTCGGATAA AGTTAAATAA AGTGTCTGAG ACGACCATCA TTCTTAATCC
 cmrCO1 Genomic DNA >
 -1129 -1119 -1109 -1099 -1089 -1079 -1069 -1059
 * * * * * * * *
 ATTTGTACIT ATCAAATTIG TATCTGAGAT TTAAAGTCAA ATTACGACTA AAAACATGGA ATGTGTGCG ACAATCACAA
 cmrCO1 Genomic DNA >
 -1049 -1039 -1029 -1019 -1009 -999 -989 -979
 * * * * * * * *
 TGGAAAATAC GTATGTGTA TICCATCACC TTTCAGTTC TAACTAGGA TATGTGTTGG AATTAITGAG ATTAAITAAA
 cmrCO1 Genomic DNA >
 -969 -959 -949 -939 -929 -919 -909 -899
 * * * * * * * *
 TTATTCCTTT ATCCGTGAC AGTTTATTTT TTGTGTTAACG ATGTGTGTA GAACGACGA AATATGTGAT TAAACCAAGA
 cmrCO1 Genomic DNA >
 -889 -879 -869 -859 -849 -839 -829 -819
 * * * * * * * *
 TCGCATACAA ATAAGAGCTA GATCCTAAAG ATATATAAAA GTATGTCAA CAACGTCACAA AACGTTCTT TTCGATGTA
 cmrCO1 Genomic DNA >
 -809 -799 -789 -779 -769 -759 -749 -739
 * * * * * * * *
 ATTATCTTAA GAACTTCAG GTTAAATTAG ATCTCTTAAAT TAAAAAAAT CATAGTAAAT GCATCCTGTA ACAAGAAAAA
 cmrCO1 Genomic DNA >
 -729 -719 -709 -699 -689 -679 -669 -659
 * * * * * * * *
 ACATAAAGAA CCCATGGTG TCTTAATTT TGTAGTAAAT AAGCGTAGTT CAAGACACAA GTAAGAATGA CGTTACCA
 cmrCO1 Genomic DNA >
 -649 -639 -629 -619 -609 -599 -589 -579
 * * * * * * * *
 TGTTAACTTA GATTCCAAA CTTGAGCTTG AGRCACGTT ACGAAAATTA TCTACGAAAA CGAGTAAGTC GTCTAAGTTC
 cmrCO1 Genomic DNA >
 -569 -559 -549 -539 -529 -519 -509 -499
 * * * * * * * *
 GTTTTCGTTT ATTTGACACG TAAGATACTC GTTATGAAAG AAGACGAAA ATGGAAAAAA GTAAAGAAGG TAAGGAGTG
 cmrCO1 Genomic DNA >

Fig. 2A

-489 -479 -469 -459 -449 -439 -429 -419
 * * * * * * * *
 GGTGAGTCCA AAGGAAACAT ACCAANTCA TGCAAGAACT ATGGAGATICA GAAATTAAGA GAAAAGTCG GAAATCATGT
 cm⁴C01 Genomic DNA
 >

-409 -399 -389 -379 -369 -359 -349 -339
 * * * * * * * *
 AACTAAATT AAAATACATA TAGGTACTAT TTTCCTTCTT TTTCCTATGAA ASRAAGAGA NNAAGGGGA ATTAGNGTAT
 cm⁴C01 Genomic DNA
 >

-329 -319 -309 -299 -289 -279 -269 -259
 * * * * * * * *
 ATGCCATTTG CAGACATAAA ATAATAANAG TTAATTCAAA TTGGGTCCA AACTCACCAA AGAGGAAATT CAGIGITGA
 cm⁴C01 Genomic DNA
 >

-249 -239 -229 -219 -209 -199 -189 -179
 * * * * * * * *
 TAAAGCCAT TAGCCAAAGC CAAAGCCAA GCGACCTCTT CTCTTCTTCA CATACATGCA TGAAATTCA TGGGCCATT
 cm⁴C01 Genomic DNA
 >

-169 -159 -149 -139 -129 -119 -109 -99
 * * * * * * * *
 CTCTTCTCA TCACATTTT ATAATTTTA TCTCTCTCTT CTCTCTCTC TCTCTCTCTT CTCTCTCTC
 cm⁴C01 Genomic DNA
 >

transcriptional start site in Tomato E4
 -89 -79 -69 -59 -49 -39 -29 -19
 * * * * * * * *
 TATA box
 TTCTTTTTT ATCAATTTC TTCCCACTTT CCATCTCAA ATAATTTCA CTATAATAC CCCCTCTTAA TAATCTGTC
 cm⁴C01 Genomic DNA
 >

-9 | 2 12 |
 * |* * |
 translational start site
 BamH1
 CAACACACCC AGGATCCATT ATTAGAGATT GAGCC ATGG
 cm⁴C01 Tom E4 5'UTR

Fig. 2B

NEB 1233
 -1669 -1659 -1649 -1639 -1629 -1619 -1609 -1599
 * * * * * * * *
 AGCCGATAAC AATTCACACAG AGGAAACAGC TATGCCATTG ATTACCCCA GCTTGTGATT GAGCTCGGTT CCACTAGTAA
 HindIII -BamHI-
 Lac promoter >
 pCR2.1 >
 -1589 -1579 -1569 -1559 -1549 -1539 -1529 -1519
 * * * * * * * *
 CGGGCGCGAG TGTGCTGGAA TTGGCTTGAT AATACGATTC ACTATAGGGC ACGCGTGGTC CACGGCGCGG GCCTGGTAAC
 pCR2.1 >
 GenomeWalker Adaptor >
 -1509 -1499 -1489 -1479 -1469 -1459 -1449 -1439
 * * * * * * * *
 AGAAGCTAAA GGAGGAAGC AACATANITA AAATTAATCC AAGATANITA AAATAAAAAA TATCTATAT TTTATGGCT
 MEL7 promoter >
 -1429 -1419 -1409 -1399 -1389 -1379 -1369 -1359
 * * * * * * * *
 TACATCTTCC TTTCCTCTTC TCTCTTCTTC TCGCGGATT TCTCCCATC TATTCTCTCT TTTCACCTTA TTTTCTCTTC
 MEL7 promoter >
 -1349 -1339 -1329 -1319 -1309 -1299 -1289 -1279
 * * * * * * * *
 TACATGTGTT AGMTTGGGT AACCAAATCT GATTCCTTC TATCGCTTT CTCTCTTC TCCTTTTTT TCGCGTGGAA
 MEL7 promoter >
 -1269 -1259 -1249 -1239 -1229 -1219 -1209 -1199
 * * * * * * * *
 TTCTCTCCA TIGCTATGG TTTTCTTCCT TTCTCTTCTT TACATGTTA CCAAATCTAA AAGATGTTT ATAAGAACCT
 MEL7 promoter >
 -1189 -1179 -1169 -1159 -1149 -1139 -1129 -1119
 * * * * * * * *
 TTCAAAAAA AAAATGTGTT AGATTTGGGT AGCCAAATTT AAACATGCG GTAAAAAAA TAAAGATGCG TAGACAANTC
 MEL7 promoter >
 -1109 -1099 -1089 -1079 -1069 -1059 -1049 -1039
 * * * * * * * *
 TAAACGATG TGCCACAAAAA GATTAAAAAA ANTCTTGTG TCAACTCTAA ACANTGTAT ACCAAAMITA AACGATAGAA
 MEL7 promoter >
 -1029 -1019 -1009 -999 -989 -979 -969 -959
 * * * * * * * *
 TTGAATTAAT AAAATGGGT GATTGGCTA TCCAAATTAA ANTGCACAAA TCTAAAGAT CGTATACCAA ATCTAAACGA
 MEL7 promoter >

Fig. 3A

-949 -939 -929 -919 -909 -899 -889 -879
 * * * * * * * *
 TOGKATACCA AATCTAAATG ATCATGTACCC AATATTTATAA TGCACATGTG TGGCAGGGTG GTTGAACGGAA CATTTCATAT
 MEL7 promoter >

 -869 -859 -849 -839 -829 -819 -809 -799
 * * * * * * * *
 ATTTCTATTT ATGGGTTTGT AGAATTTTTT CATTTTGGAA ATGGTCTAT ACAATATAAA TTTAAATTTT TTACCACTTC
 MEL7 promoter >

 -789 -779 -769 -759 -749 -739 -729 -719
 * * * * * * * *
 GTTATTTT CGAAAAGGCC CCTTAATAA ATTGAATTCG CTATATAA AAATTTTTC CGAAAAAAAG TAGACTATG
 MEL7 promoter >

 -709 -699 -689 -679 -669 -659 -649 -639
 * * * * * * * *
 CTAATCTAAA ATTGGATTC CAATATAGAA CAAATCTCA AAATGAACAA ACATTTGAA TCTCGATAT AGAAAACNT
 MEL7 promoter >

 -629 -619 -609 -599 -589 -579 -569 -559
 * * * * * * * *
 TACTTATTTT GAATGGGAC ATATTCAAA GTTATCTCA AAOGTAACTT TGAGGAAAA GTTGTGAG ATTACATCCA
 MEL7 promoter >

 -549 -539 -529 -519 -509 -499 -489 -479
 * * * * * * * *
 TATTTTGTG TTCTCATTTG ATTTCATGG AATTTTAAA TGCACACAAA ATGGTGTATG AGTTAACCC AATGTTTAC
 MEL7 promoter >

 -469 -459 -449 -439 -429 -419 -409 -399
 * * * * * * * *
 GITATTGAAAT CTCTTATTA AAAACCAAC AAAATTTAA AACTGTTTG CAATAGACCA ATATAGTAA TCCATCGTG
 MEL7 promoter >

 -389 -379 -369 -359 -349 -339 -329 -319
 * * * * * * * *
 TCTATGTTG ATTAATGTA ATATTTGTT ATATTAATAA AATATTTGA TTATTTGAA TATATTGTTA TTGAGACAT
 MEL7 promoter >

 -309 -299 -289 -279 -269 -259 -249 -239
 * * * * * * * *
 AAAATTAAGA TTAAATTAATTTT ATTATATATTC TTAAATTAATTA CATTGTTAA TTCTCTTATTTAGACCAT TTCTCTTAT
 MEL7 promoter >

 -229 -219 -209 -199 -189 -179 -169 -159
 * * * * * * * *
 TTATATATAAC ATTTTAATAAA CTAATGATG TGACACACAC TAAATTTATT TTATCCAAA GAAAATTAAG CTTATAAAATA
 MEL7 promoter >

Fig. 3B

-149 -139 -129 -119 -109 -99 -89 -79
 * * * * * * * *
 TGGGCTCTCT TTATCACCCTT CATGATAATT ATGAAAAAAA AAATAAAATT TAATTATATA ATTICATTTC A TCAATATGDA
MEL7 promoter >

-69 -59 -49 | -39 -29 -19 -9 2
 * * * | * * * * *
 CAAGCTAGAT ATTACTATAT CAACAACCTT GIGITATAAAA AGGGCAAGAA ATTAGCATT ATGTGTGAG CCACCTTTTC
MEL7 promoter >

MEL7 translational start site
 |
 <cmDruNcoSt
 12 22 32 42 | 52
 * * | * * *
 TATATCTAGA GATAGAAGGT TTAAATCTAT GTCTCTAATT GGAAAGCTTG TGAGT
 TTCCA ATTTCGTA CcGAGATAA CCTTTTG
-NcoI-
MEL7 promoter >

MEL7 cds >

Fig. 3C

NEB 1233

|

-2158 -2148 -2138 -2128 -2118 -2108 -2098 -2088
 * * * * * * * *

TGTGTTGGAA TTGTGAGCGG ATAACAATT CACACAGGAA ACAGCTATGA CCATGATTAC GCGAACGTTG GTACCGAGCT
 pCR2.1----->

Lac promoter ----->

-2078 -2068 -2058 -2048 -2038 -2028 -2018 -2008
 * * * * * * * *

CGGATCCACT AGTAACGCC CGCAGTGTC TGGAATTGGG CTTACTATAG GGCACCGGTC GTGAGCGGCC CGGGCIGGTC
 -SpeI---
 pCR2.1----->

GenomeWalker Adaptor ----->

-1998 -1988 -1978 -1968 -1958 -1948 -1938 -1928
 * * * * * * * *

CANTCACOGA ACNTCATGTT ATGAGGTGT CGGAGATGC TACCTATCTG CTGATGTTGG TTTCTTTCCT TGAAAGATAC
 MEL2 promoter----->

-1918 -1908 -1898 -1888 -1878 -1868 -1858 -1848
 * * * * * * * *

TCCTCCTGACT TTITAGTTGT TCCATCTAGA GATGCTCTCT ATTATTTTGA CACCTTTCT TCTGACGGTG TAGAGCAACA
 MEL2 promoter----->

-1838 -1828 -1818 -1808 -1798 -1788 -1778 -1768
 * * * * * * * *

CAAAAATC TTGATTTCT ATTAATGAA TGAGCTATAT CTATACAAAT TGGACACATA TGACAAATTA AGAAAGMTTC
 MEL2 promoter----->

-1758 -1748 -1738 -1728 -1718 -1708 -1698 -1688
 * * * * * * * *

TTTCGAAATA TTATGCAATA GAATACTCA CCAGGTTAA TGATGCACT TATAGAGAAA ACTTOGAGA ACAAGAGAC
 MEL2 promoter----->

-1678 -1668 -1658 -1648 -1638 -1628 -1618 -1608
 * * * * * * * *

GCTACTAAGT TTATGAGAA TGGGTATTTC TGACCTACTA TGTTTCAGGA TGGAGGAGTC TTATGGCTCA ATTGTTGAGCG
 MEL2 promoter----->

-1598 -1588 -1578 -1568 -1558 -1548 -1538 -1528
 * * * * * * * *

ATGGGGAGGA ACTGAAATA TTTCCTATCT CAATGAAATA CTAACACAC ATATCCTAGA GGTTGAACTA TTGTATATCT
 MEL2 promoter----->

-1518 -1508 -1498 -1488 -1478 -1468 -1458 -1448
 * * * * * * * *

AGGAAATACA TTTTATGGAA CGCGTTTCTA GTTGTTCGG CAACACAGCA TTGAGAGCG GACGTTCTAG TOGCATACCA
 MEL2 promoter----->

Fig. 4A

-1438 -1428 -1418 -1408 -1398 -1388 -1378 -1368
 * * * * * * * *
 OGGAGGATCC GCGATGTAAGC TATGCCAAGCA ATACCTCTCAC CCTTTTGTGC TCTCTTATAA ATATATTTTT TACTTACTAA
MEL2 promoter >

 -1358 -1348 -1338 -1328 -1318 -1308 -1298 -1288
 * * * * * * * *
 GATAGTTCT AAATTGTTTG TAGAACATCGAA TGCTGGAACT TOAGTCCTAG CTACCTCAG TGGGTACTTA GCCACTCT
MEL2 promoter >

 -1278 -1268 -1258 -1248 -1238 -1228 -1218 -1208
 * * * * * * * *
 GGGGACAAGA TATGOGAGAT GCGCGITGGAT AGACGATTTGG ACTACTAAAG AGGCGTTGGT TGGGGACCTA AGCTCTAGGC
MEL2 promoter >

 -1198 -1188 -1178 -1168 -1158 -1148 -1138 -1128
 * * * * * * * *
 CCACAAAGCG CGCAAGTGTGA GTAGTTCCAC GACCTCAAGT TTGTAGTCGA OGGTAGAGCT CCAGTTATGG ACTAAGCTTG
MEL2 promoter >

 -1118 -1108 -1098 -1088 -1078 -1068 -1058 -1048
 * * * * * * * *
 ATCAAAGCTGT GCAACGGATT GAAGAACAAA CAAGAAATCA CGATGGCTTA GCTTCAAAAG TGGAAATGAAT GTGAAAGTC
MEL2 promoter >

 -1038 -1028 -1018 -1008 -998 -988 -978 -968
 * * * * * * * *
 ATAGAAAGACA TGAGTOGGCC ACAGTAAAGGA CCACACATTT ATCTTAACTT TTGGCGTACG TMTANNTATT TCCMTTATTC
MEL2 promoter >

 -958 -948 -938 -928 -918 -908 -898 -888
 * * * * * * * *
 TTAAAGTTTT GAACTTACAGT ATTCAGTGTAT GATAATGCAAT TATATGTAAC AAAAGTAGCC ACTTTTGATAT AATTTGAGGA
MEL2 promoter >

 -878 -868 -858 -848 -838 -828 -818 -808
 * * * * * * * *
 CCTGTGGGTG AGAAATGGCAT ATGAGGGCTCG TTAAAGACAA TACGTTTTCCTT TTGTGCTTT TTTTAACAGG GAMATTTTT
MEL2 promoter >

 -798 -788 -778 -768 -758 -748 -738 -728
 * * * * * * * *
 TATTTTGATAT ATGAACTTTA TTACATTCTT TGAATTCTT TGTATTTATGA AGATTTAATT TTTTGTGAA TTTTTGTTTG
MEL2 promoter >

 -718 -708 -698 -688 -678 -668 -658 -648
 * * * * * * * *
 TATTTTGATAA TTTACTTAATT TATTTTAAAT TTTCCTTAAAT TGAATCGATA ACCAATGCAA ATATTTTACG AAAAAAAACT
MEL2 promoter >

Fig. 4B

-638 -628 -618 -608 -598 -588 -578 -568
 * * * * * * * *
 ATAGGAAT ATTCAAAAA AATAAAAAT TACATATTTT AAATATTTT CGACGCTTA CATACTGGG AAATAAGGG
 MEL2 promoter >

 -558 -548 -538 -528 -518 -508 -498 -488
 * * * * * * * *
 CAACATCAC ATCGGGGTG GTTATTACCG ACCCATGRAT GACACOGAAT ATATAAACGT AAGGANTAGT TAATCCCTGAC
 MEL2 promoter >

 -478 -468 -458 -448 -438 -428 -418 -408
 * * * * * * * *
 GCATAACTGC TGTCGGAACG GTGGAAGTTA GTTCTGACAA TTATTAACAC TTACGTGAC GTTTTATGC ATCGGGAGTC
 MEL2 promoter >

 -398 -388 -378 -368 -358 -348 -338 -328
 * * * * * * * *
 GCTCCACTTC TTGTTAGTGA GAATTTTGC CTATAAATGC GGTTTAAAC CGACATTAAC GGCCTAAATT CTCTTAGTGC
 MEL2 promoter >

 Imperfect inverted repeat
 -318 -308 -298 -288 -278 -268 -258 -248
 * * * * * * * *
 ATAATCANTA TMCAAAAGTT CAATTCAAA AATTACATTT CTCCTGAAATC TCCGTGIGAA CAATGTGCTA AAAGGTTTAA
 MEL2 promoter >

 -238 -228 -218 -208 -198 -188 -178 -168
 * * * * * * * *
 AGTGATGATGA AAMTTTCAAA ACCTTAATTCG ATTACCGAG AAMTTTATTT TAATCCTCAT TCAAAGGTTA TTAACTATGA
 MEL2 promoter >

 -158 -148 -138 -128 -118 -108 -98 -88
 * * * * * * * *
 AAAATATGGA AGATTAAGATT TCAAATTTAC GTAAATTACG TCTACGGTTT TTTCCTTCCC CTTPAGTAAC TTCACCTATA
 MEL2 promoter >

 TATA box
 | -78 -68 -58 -48 -38 -28 -18 -8
 | * * * * * * * *
 TCTTTATA CGTTCATCC CTTCACATTC TCATACAAA TTCTCTTCA ATATCAACTC TCTCTCTTA ACTCACCCCT
 MEL2 promoter >

 MEL2 translational start site
 | <MEL2_Nco_R
 1 3 13
 * * * |
 TTTCACATG GAAACATGC AAAC
 AAAGggTAC CTTTGTACG TTTG
 -NcoI--
 pro |
 MEL2 cds

Fig. 4C

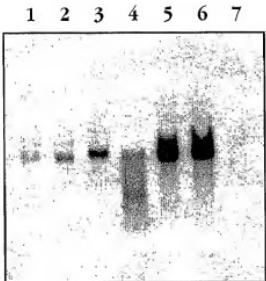


Fig. 5A

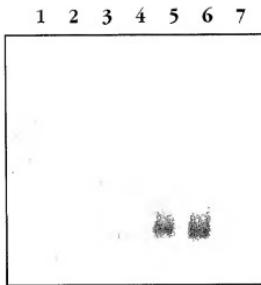


Fig. 5C

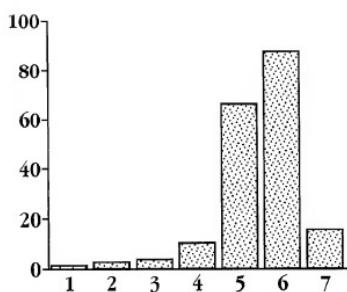


Fig. 5B

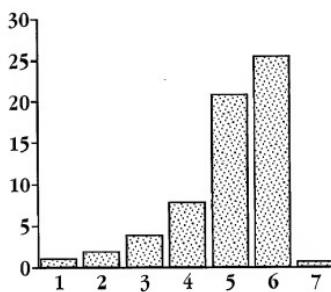


Fig. 5D

-968 -958 -948 -938 -928 -918 -908 -898
 * * * * * * * *
 TGGAAATTGTC AGOGGATAAAC AATTTCACACG AGGAAACAGC TATGACCATG ATTACGUCAA GCTTGGTACG GAGCTGGAT
 BamHI>
 _____ pCR2.1 _____>
 Lac promoter _____>
 -888 -878 -868 -858 -848 -838 -828 -818
 * * * * * * * *
 CCACTAGTAA CGGGCGCCAG TCTCTCTGGA TTGGCTTAC TATAGGGCAC GGTGGTCA GA CGGCCCCGGC TGTTAATT
 pCR2.1 _____>
 _____ GenomeWalker Adaptor _____>
 -808 -798 -788 -778 -768 -758 -748 -738
 * * * * * * * *
 TGAAGATTA GGAGNTATTT TTTCATATA AGAGNTATTT TTNTNTATGT AACNTNTTTT TTACTAGACG GTTGAGTCGA
 6E melon genomic DNA _____>
 -728 -718 -708 -698 -688 -678 -668 -658
 * * * * * * * *
 GTTGGTTAA AGAAAGAAA ACTNTAAAT AATTNTAAAT TTTAANTAC ATAAACAATA CTTTGTATC TATTTAANT
 6E melon genomic DNA _____>
 -648 -638 -628 -618 -608 -598 -588 -578
 * * * * * * * *
 AAAATGACTA TTGAATGTT AAGATGTTAGG TATCTAAGGA CAAAGACTCT OGAGTTCAA TCTTCAACTT CAANATATAC
 6E melon genomic DNA _____>
 -568 -558 -548 -538 -528 -518 -508 -498
 * * * * * * * *
 TGCAGATAG TAATCTATGA ATTNTATTTG ACTAAATCAT GTAGCANAAG AAATCAANT TTATCTATGTT AAATATGGTC
 6E melon genomic DNA _____>
 -488 -478 -468 -458 -448 -438 -428 -418
 * * * * * * * *
 AAGCGGAGC ATTAACACA ACAATCATA TTGTTGGTTG ATAGTACTTG ACTAGAATTT AGAGAGTACT TGACTAGAAT
 6E melon genomic DNA _____>
 -408 -398 -388 -378 -368 -358 -348 -338
 * * * * * * * *
 AAAATITGGG GGACCCACTA CGAOTICAGC TTGCTCTGT TAGCAATTA GCTATCACTT CTTAGCTAT ACCTTGTGC
 6E melon genomic DNA _____>

Fig. 6A

-328 -318 -308 -298 -288 -278 -268 -258
 * * * * * * * *
 GCTGCAATTAA ACGGTTTCTT CACACTTTTC TTTTCCTTTT ACGGCACCCG TGGGTATAAT GGCTCCCCCA CTTTTAACCT
 _____ 6E melon genomic DNA _____ >

 -248 -238 -228 -218 -208 -198 -188 -178
 * * * * * * * *
 TOCCCAGAATC CAAGCAGTT GCCAACATGC GAAGCACCPAA GTACATTAATT GTCATTTGC ATTARACAAA ATGACACGTC
 _____ 6E melon genomic DNA _____ >

 TATA
 box>

 -168 -158 -148 -138 -128 -118 -108 -98
 * * * * * * * *
 GGATGCAATT TATGTAATTA AGCTACAAAG CCACGGTTAG TTTCGGAAACCCACGATCC AGTACTTACG TGTCCTCTAT
 _____ 6E melon genomic DNA _____ >

 -88 -78 -68 -58 -48 -38 -28 -18
 * * * * * * * *
 AAATCTTAGA AGCAACGCT TTACCGGAAT CAACCTTAAG GGTATCCATT TTTCATCTAT CAATTACACC TTGAAACTCC
 _____ 6E melon genomic DNA _____ >

 6E translational start site
 |
 <6EmelNcoP
 -8 1 3 |
 * * * |
 TTTCGGGC ACAGCT ATG GCC TC
 AAAAGGGCGG aGCTGg TAC CGG A
 --NcoI--
 _____ 6E melon genomic DNA _____

Fig. 6B

卷之三

-2442 -2432 -2422 -2412 -2402 -2392 -2382 -2372
 * * * * * * * *
 AGCTTGCAT GCGTCAGGT CGACTCTAGA TCAATCAAC ATTTATTTAA ATAGAACGTT TTAGTGGTTT TGGATTTTA
 -Hind3
 pUC-19 >
 2F melon genomic DNA >
 -2362 -2352 -2342 -2332 -2322 -2312 -2302 -2292
 * * * * * * * *
 TTATCTTTT TTATTAATTA CATTCAATT AGATTTAAT CTTCAGAGG ATGGAGGAG AGAAATTATA GAAATGAC
 2F melon genomic DNA >
 -2282 -2272 -2262 -2252 -2242 -2232 -2222 -2212
 * * * * * * * *
 TGAATDAGAC TTAATTTATA AAATCAAAA GAAATGGT GCGAACANG GIGACTAAGA GTGTATGAA TTGAAATTAG
 2F melon genomic DNA >
 -2202 -2192 -2182 -2172 -2162 -2152 -2142 -2132
 * * * * * * * *
 AACATTCCTT CTGTATAGAT ATTAATGATG TTTCTCTTA CTTTATTTTTT ATGGGGTTA TTTATTAATA ACTGAATTIT
 2F melon genomic DNA >
 -2122 -2112 -2102 -2092 -2082 -2072 -2062 -2052
 * * * * * * * *
 TAAGAGTCTT TTATTAACC AATGTTATA GGATTCATT GATGTTTTA TGAGATTAGG CAACACATT ATTATGAGA
 2F melon genomic DNA >
 -2042 -2032 -2022 -2012 -2002 -1992 -1982 -1972
 * * * * * * * *
 AATAATTTAG TGTAGAAAGT AATTTCATT TTGGATTTGT TAGATGAAAC TCAAATCTG CAACAACATT CAGTTAAGTA
 2F melon genomic DNA >
 -1962 -1952 -1942 -1932 -1922 -1912 -1902 -1892
 * * * * * * * *
 TATATAATAA TATAGAGCCA CCAACCTAA ATACAATATC TTGCGAGCA AAATTTATA CATAATATGG AAAAGAGT
 2F melon genomic DNA >
 -1882 -1872 -1862 -1852 -1842 -1832 -1822 -1812
 * * * * * * * *
 AGTACTGGTA CATGAATCTT ACCGAGAATT TAAGTATTT TGCGTTTTCG AATOCAGAG TCTCAACAAA TCACATTITA
 2F melon genomic DNA >
 -1802 -1792 -1782 -1772 -1762 -1752 -1742 -1732
 * * * * * * * *
 AAAACCGATT GAAATACAT GCAAGTAAGA CTTTGAAAAA AACAAAGCTT CAACCTCTAT ATCAATTTAC TCTATATGCA
 2F melon genomic DNA >
 -1722 -1712 -1702 -1692 -1682 -1672 -1662 -1652
 * * * * * * * *
 AACATGTTAGG TCAAATGAGT ATGAAATTA AGGAGCAATC ACTAATAAA AATCAATATA GTGAATGCA AAGAAACAA
 2F melon genomic DNA >

Fig. 7A

2F melon genomic DNA

-1642	-1632	-1622	-1612	-1602	-1592	-1582	-1572
*	*	*	*	*	*	*	*
TATCAATCAA ACCTTAATGTA TACGIGGATG ATGATGCACT GIGITTTTGAG ATATGGACAT TTGATAAAC AACAAACCTC _2F melon genomic DNA >							
-1562	-1552	-1542	-1532	-1522	-1512	-1502	-1492
*	*	*	*	*	*	*	*
CACTCAATA CGGGAAGAGA GGCATTTGAGT GACAGTTAG TGCCCTATIG AGAGGGTAA GTCCAAAMCA AAACAAACAC _2F melon genomic DNA >							
-1482	-1472	-1462	-1452	-1442	-1432	-1422	-1412
*	*	*	*	*	*	*	*
AAAACATGTT GAAGAATGTT TATGAAATAA TGGCAGGGAA AGACATGGGT GTACATGTTG TGAGGTTT CTCTCTTCAA _2F melon genomic DNA >							
-1402	-1392	-1382	-1372	-1362	-1352	-1342	-1332
*	*	*	*	*	*	*	*
ATCITGTAAT AATTTGGATT AGGACCCAAAC AAGAGAAACA CTTGTTGGAA ACCATGACAG GGCTAACCCA TGGGTGAAT _NcoI— >							
-1322	-1312	-1302	-1292	-1282	-1272	-1262	-1252
*	*	*	*	*	*	*	*
ATCAGTATT TAATTAATTA AGCCTCTAC CCGGCCATTG GTTTTTTTTG TCGATTCAATA TCITTTTTTTT TATTTACGAA _2F melon genomic DNA >							
-1242	-1232	-1222	-1212	-1202	-1192	-1182	-1172
*	*	*	*	*	*	*	*
TAATTCCTGA GTTGTGATTIC AATTTAGTCG GTCTATAGTA ATATTTTAAA CTTATGTTAAT ATATAAAAGG TAATGGGAA _2F melon genomic DNA >							
-1162	-1152	-1142	-1132	-1122	-1112	-1102	-1092
*	*	*	*	*	*	*	*
TGATTCTTAAT AGTATTCACT TTATATCACT CCTTCCTTAGA GTAAAGTTT TAAAGTGGGA AGGGAAATGG ATATCGACGT _2F melon genomic DNA >							
-1082	-1072	-1062	-1052	-1042	-1032	-1022	-1012
*	*	*	*	*	*	*	*
GTGATGGTA GTTAATTTTC CTTATCGACG AGGTTCTGT TCCCTTACTT ATATATATGG AGTCATCCTC AATTTTCCAA _2F melon genomic DNA >							
-1002	-992	-982	-972	-962	-952	-942	-932
*	*	*	*	*	*	*	*
CCTCTCAACTT CCTTAATTTAC AAGCAAAACA TTCAATPACCA TACATGCACT TTITTAGAAA GAAAAGAGT TCCTCTTGG _2F melon genomic DNA >							
-922	-912	-902	-892	-882	-872	-862	-852
*	*	*	*	*	*	*	*
ACTTTTTTT TCAATICAAC TATGCCACCTT TGTATTTATAAT TTGTTGTTT TCTTCGTTT AATCAAGTIG _2F melon genomic DNA >							

Fig. 7B

-842 -832 -822 -812 -802 -792 -782 -772
 * * * * * * * *
 TTGTAATCRA CTTTATGAT TCAAACACNT AGATATTG TTTAATAGTA TCAGTATATA ATAGGGTAG AATAACCCTT
 2F melon genomic DNA >

-762 -752 -742 -732 -722 -712 -702 -692
 * * * * * * * *
 CAATATGIG TTTTAAANAA ATCAAAATCAC TTTAAARNTT AAAATAITGT TAATTAAGTGT AITGTTTCTT TTTTAAGTAT
 2F melon genomic DNA >

-682 -672 -662 -652 -642 -632 -622 -612
 * * * * * * * *
 TAAACCCAGA TAAAAAGTGC TTTAACACTT ATAAAAAARTT AGATTTATTT AAAGGAAGTT GTCTGAACGG CAAAATGAC
 2F melon genomic DNA >

-602 -592 -582 -572 -562 -552 -542 -532
 * * * * * * * *
 AAATATPAAC AAAGTTTAAAT GACATGTTT CGAAATGTTT CGAAGAGGAA AGAAACATT AAGTTGAAA TATCTOGAGT
 2F melon genomic DNA >

-522 -512 -502 -492 -482 -472 -462 -452
 * * * * * * * *
 TAAATACATA TCATCCCCATA GTATATATA ACAAAAACAA CCTAAATCIG AAAAATTAAT TGATGTAAAT AAGAAAAAGA
 2F melon genomic DNA >

-442 -432 -422 -412 -402 -392 -382 -372
 * * * * * * * *
 GATCAACIC TTAATTTTTT AAAAATTAAC TGGTGAAAAA ARCTGAATAA TTTCATTAAT TGTTTAATTTT CAAATGAC
 2F melon genomic DNA >

-362 -352 -342 -332 -322 -312 -302 -292
 * * * * * * * *
 CAAAATTA AGITAAAAAA GCATTAACAA AAACATICA AACCTAGCT ACTACACATT TAGGRAAATA TATGATACAC
 2F melon genomic DNA >

-282 -272 -262 -252 -242 -232 -222 -212
 * * * * * * * *
 AAAGGTTTT TGCGGTTAAA CATCTTTTAT ATTTCATATA ACCAACACTT CGTATATATA CACACATAAA GAAGGAAAAA
 2F melon genomic DNA >

-202 -192 -182 -172 -162 -152 -142 -132
 * * * * * * * *
 GAATTAATGC AAGGGTGTGG CCATTAACGT ACCGCGOGICA TATCCATACAT ATCCGTTAG TCTCAAAATC TCTCTCTCTC
 2F melon genomic DNA >

-122 -112 -102 -92 -82 -72 -62 -52
 * * * * * * * *
 CCTGCCTCIC TAATTATTC TGCCAGOGAC CATAATTCTAT TTCTAAATGTT GIGTTAAAA AGCCGAGAAT CGCAATCCCT
 2F melon genomic DNA >

Translational start site
 -42 -32 -22 -12 -2 |
 * * * * * |
 TTCCCTCCAC TCTTAATTC TTTCCATTC ACAAAAAT A G GATCGGCCAC CAGGG
 -BamHI- -NcoI-

Fig. 7C

6E 2F melo Acol mel7 mCTR SAMase melo actin 18S

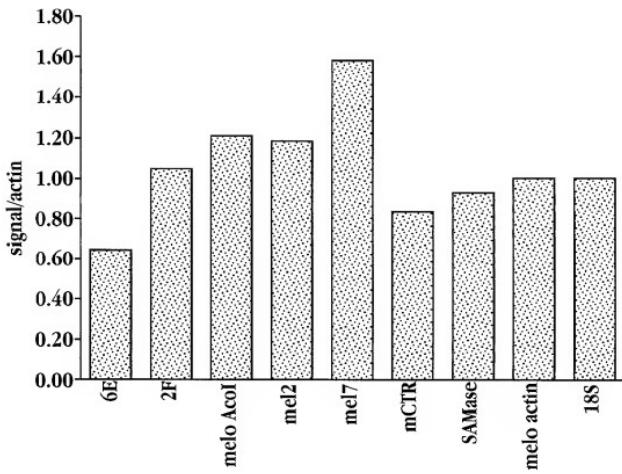


Fig. 8